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NEWS	4	JUN		USPATFULL and USPAT2 updated with 11-character
HEND	-1	0011	10	patent numbers for U.S. applications
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NEWS	6	JUN	25	CA/CAplus and USPAT databases updated with IPC
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NEWS		JUL		CA/CAplus patent coverage enhanced
NEWS	12	JUL	28	EPFULL enhanced with additional legal status
				information from the epoline Register
NEWS		JUL		IFICDB, IFIPAT, and IFIUDB reloaded with enhancements
NEWS		JUL		STN Viewer performance improved
NEWS		AUG		INPADOCDB and INPAFAMDB coverage enhanced
NEWS	16	AUG	13	CA/CAplus enhanced with printed Chemical Abstracts
				page images from 1967-1998
NEWS		AUG		CAOLD to be discontinued on December 31, 2008
NEWS		AUG		CAplus currency for Korean patents enhanced
NEWS	19	AUG	27	CAS definition of basic patents expanded to ensure
				comprehensive access to substance and sequence
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NEWS	20	SEP	18	Support for STN Express, Versions 6.01 and earlier,
			0.5	to be discontinued
NEWS	21	SEP	25	CA/CAplus current-awareness alert options enhanced
				to accommodate supplemental CAS indexing of
NEWS	22	SEP	0.0	exemplified prophetic substances
NEWS	22	SEP	26	WPIDS, WPINDEX, and WPIX coverage of Chinese and
NEWS	22	SEP	20	and Korean patents enhanced IFICLS enhanced with new super search field
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NEWS	24	SEP	49	display fields
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NEWS 25 SEP 30 CAS patent coverage enhanced to include exemplified prophetic substances identified in new Japaneselanguage patents

NEWS 26 OCT 07 EPFULL enhanced with full implementation of EPC2000 NEWS 27 OCT 07 Multiple databases enhanced for more flexible patent number searching

NEWS 28 OCT 22 Current-awareness alert (SDI) setup and editing enhanced

NEWS 29 OCT 22 WPIDS, WPINDEX, and WPIX enhanced with Canadian PCT Applications

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3, AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

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=> 11 L2

10 L1

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(PD<20040113) 4 L2 AND (PD<20040113) T. 3

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L3 ANSWER 1 OF 4 HCAPLUS COPYRIGHT 2008 ACS on STN ACCESSION NUMBER: 2003:130956 HCAPLUS

DOCUMENT NUMBER: 138:199733

TITLE: A Drosophila full-length cDNA resource

AUTHOR(S): Stapleton, Mark; Carlson, Joe; Brokstein, Peter; Yu, Charles; Champe, Mark; George, Reed; Guarin, Hannibal; Kronmiller, Brent; Pacleb, Joanne; Park, Soo; Wan,

Ken; Rubin, Gerald M.; Celniker, Susan E.

CORPORATE SOURCE: Berkeley Drosophila Genome Project, Lawrence Berkeley

National Lab., Berkeley, CA, USA

GenomeBiology (2002), 3(12), No pp. given

CODEN: GNBLFW; ISSN: 1465-6914

URL: http://genomebiology.com/content/pdf/gb-2002-3-12-

research0080.pdf

PUBLISHER: BioMed Central Ltd.

DOCUMENT TYPE: Journal; (online computer file)

LANGUAGE: English

A collection of sequenced full-length cDNAs is an important resource both for functional genomics studies and for the determination of the intron-exon structure of genes. Providing this resource to the Drosophila melanogaster research community has been a long-term goal of the Berkeley Drosophila Genome Project. The Drosophila Gene Collection (DGC) has been previously described , a set of putative full-length cDNAs that was produced by generating and analyzing >250,000 expressed sequence tags (ESTs) derived from a variety of tissues and developmental stages. High-quality full-insert sequence were generated for 8921 clones in the DGC. The sequences of these clones were compared to the annotated Release 3 genomic sequence, and >5300 cDNAs identified that contain a complete and accurate protein-coding sequence. This corresponds to at least one splice form for 40% of the predicted D. melanogaster genes. Potential new cases of RNA editing were also identified. Thus, comparison of cDNA sequences to a high-quality annotated genomic sequence is an effective approach to identifying and eliminating defective clones from a cDNA collection. Clones were eliminated either because they carry single nucleotide discrepancies, which most probably result from reverse transcriptase errors, or because they are truncated and contain only part of the protein-coding sequence. [This abstract record is one of five records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

481877-77-4

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; full-length cDNA sequence resource for Drosophila melanogaster)

481877-77-4 HCAPLUS

RE68566p (Drosophila melanogaster strain v; cn bw sp gene CG13893) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L3 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2002:678785 HCAPLUS

DOCUMENT NUMBER: 137:380859

TITLE: R391: a conjugative integrating mosaic comprised of phage, plasmid, and transposon elements

AUTHOR(S): Boltner, Dietmar; MacMahon, Claire; Pembroke, J. Tony;

Strike, Peter; Osborn, A. Mark

CORPORATE SOURCE: Department of Biological Sciences, University of

Essex, Colchester, CO4 3SQ, UK

SOURCE: Journal of Bacteriology (2002), 184(18),

5158-5169

CODEN: JOBAAY; ISSN: 0021-9193

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

The conjugative, chromosomally integrating element R391 is the archetype of the IncJ class of mobile genetic elements. Originally found in a South African Providencia rettgeri strain, R391 carries antibiotic and mercury resistance traits, as well as genes involved in mutagenic DNA repair. While initially described as a plasmid, R391 has subsequently been shown to be integrated into the bacterial chromosome, employing a phage-like integration mechanism closely related to that of the SXT element from Vibrio cholerae 0139. Anal. of the complete 89-kb nucleotide sequence of R391 has revealed a mosaic structure consisting of elements originating in bacteriophages and plasmids and of transposable elements. A total of 96 open reading frames were identified; of these, 30 could not be assigned a function. Sequence similarity suggests a relationship of large sections of R391 to sequences from Salmonella, in particular those corresponding to the putative conjugative transfer proteins, which are related to the IncHI1 plasmid R27. A composite transposon carrying the kanamycin resistance gene and a novel insertion element were identified. Challenging the previous assumption that IncJ elements are plasmids, no plasmid replicon was identified on R391, suggesting that they cannot replicate autonomously.

476016-57-6

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; R391, a conjugative integrating mosaic comprised of phage, plasmid, and transposon elements)

RN 476016-57-6 HCAPLUS

CN Protein (Providencia rettgeri mobile element R391 255-amino acid) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: THERE ARE 74 CITED REFERENCES AVAILABLE FOR THIS 74 RECORD, ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 4 HCAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2002:173239 HCAPLUS

DOCUMENT NUMBER: 136:396932

Reagents and kits, such as nucleic acid arrays, for TITLE: detecting the expression of over 10,000 Drosophila

genes

INVENTOR(S): Venter, J. Craiq; Adams, Mark; Li, Peter W. D.; Myers,

Eugene W.

PATENT ASSIGNEE(S): PE Corporation (NY), USA

SOURCE: PCT Int. Appl., 21 pp. CODEN: PIXXD2

Patent

DOCUMENT TYPE: LANGUAGE: English

FAMILY ACC. NUM. COUNT: 10

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. A2 20010927 WO 2001-XG9231 20010323 <-------WO 2001071042 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,

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HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
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             YU, ZA, ZW
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
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             RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,
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PRIORITY APPLN. INFO .:
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                                                              P
                                                                  19991228
                                            US 2000-175693P
                                                               P 20000112
                                           US 2000-184831P
                                                               P 20000224
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- AΒ The present invention is based on the sequencing and assembly of the Drosophila melanogaster genome. The present invention provides the primary nucleotide sequence of a large portion of the Drosophila melanogaster genome in a series of genomic and predicted transcript sequences. This information is provided in the form of genomic, transcript and protein sequence information and can be used to generate nucleic acid detection reagents and kits such as nucleic acid arrays. Primary sequences are provided as contiguous strings in a computer-readable format and recorded on media such as floppy disks, hard disks, magnetic tape, CD-ROM, RAM, ROM and hybrids of these categories. Genes/exons can be predicted, sequences can be edited and homol, searches of target motifs can be conducted. [This abstract record is one of ten records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
- TT 431288-23-2 RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(amino acid sequence; reagents and kits, such as nucleic acid arrays, for detecting the expression of over 10,000 Drosophila genes)

RN 431288-23-2 HCAPLUS

Protein (Drosophila melanogaster clone WO0171042-SEOID-33039) (9CI) (CA INDEX NAME)

- *** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
- T.3 ANSWER 4 OF 4 HCAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: DOCUMENT NUMBER: TITLE: AUTHOR(S): 2000:230405 HCAPLUS 132:304167

The genome sequence of Drosophila melanogaster Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Garv H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Chervl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenva; Liang, Yong; Lin, Xiaoving; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian

P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangdun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.;

CORPORATE SOURCE: SOURCE:

PUBLISHER:

Celera Genomics, Rockville, MD, 20850, USA Science (Washington, D. C.) (2000), 287(5461), 2185-2195

CODEN: SCIEAS; ISSN: 0036-8075

American Association for the Advancement of Science Journal

DOCUMENT TYPE: Journal LANGUAGE: English

The fly Drosophila melanogaster is one of the most intensively studied organisms in biol, and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiquity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.1.

IT 262973-73-9 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; genome sequence of Drosophila melanogaster) RN 262973-73-9 HCAPLUS

CN Protein (Drosophila melanogaster gene CG13893) (9CI) (CA INDEX NAME)

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REFERENCE COUNT: 9 THERE ARE 89 CITED REFERENCES AVAILABLE FOR THIS
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481877-77-4 REGISTRY RN

RE68566p (Drosophila melanogaster strain y; cn bw sp gene CG13893) (9CI) (CA INDEX NAME)

OTHER NAMES:

GenBank AAL49263 CN

GenBank AAL49263 (Translated from: GenBank AY071641) PROTEIN SEQUENCE

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- CI MAN
- SR GenBank
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SEO
         1 MMEKCFALYR YSHSDGTAKE WAIYVGSDTO EIEVRFGKAG OMSOORLIDS
        51 TDPNAEADRR INEKINKGYR FVGQVGIDHQ GRPFELSNAL DSVACANNVS
       101 WEFRTRKDVN GQISLAQKAL FDMAKLLEAY GLAVIDDNQV RIGKWSLGFC
       151 KSGLPSTNQI SMVSGEGAGI VNTDDGPWPL LLLLAFKRQL PPLCSLTVAS
       201 PEGIEVSDQL KLEKDVLRLL GSDLERVRPI AEALDLMPAK IDLNQSSPDS
       251 QNYYF
ME
    Unspecified
CT
    MAN
SR
    CA
LC
    STN Files: CA, CAPLUS, TOXCENTER
DT.CA CAplus document type: Journal
RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)
               1 REFERENCES IN FILE CA (1907 TO DATE)
               1 REFERENCES IN FILE CAPLUS (1907 TO DATE)
=> SET NOTICE LOGIN DISPLAY
```

NOTICE SET TO OFF FOR DISPLAY COMMAND SET COMMAND COMPLETED